

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/590,801  
Source: IFWO  
Date Processed by STIC: 09/06/2006

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 09/06/2006

PATENT APPLICATION: US/10/590,801

TIME: 10:25:54

Input Set : A:\082368-009500US.txt

Output Set: N:\CRF4\09062006\J590801.raw

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4 <110> APPLICANT: Nakamura, Yusuke
5     Nakagawa, Hidewaki
6     Nakatsuru, Shuichi
8 <120> TITLE OF INVENTION: EphA4 AS THERAPEUTIC TARGET OF PRC AND
9     PDACa
11 <130> FILE REFERENCE: 082368-009500US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/590,801
C--> 13 <141> CURRENT FILING DATE: 2006-08-25
13 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/003081
14 <151> PRIOR FILING DATE: 2005-02-13
16 <150> PRIOR APPLICATION NUMBER: US 60/555,809
17 <151> PRIOR FILING DATE: 2004-03-24
19 <150> PRIOR APPLICATION NUMBER: US 60/548,335
20 <151> PRIOR FILING DATE: 2004-02-27
22 <160> NUMBER OF SEQ ID NOS: 23
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 3468
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (43)..(3003)
34 <223> OTHER INFORMATION:
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38                                     Met Ala Gly Ile
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42 Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile Cys Asp Ala Val
43 5          10          15          20
45 aca ggt tcc agg gta tac ccc gcg aat gaa gtt acc tta ttg gat tcc      150
46 Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr Leu Leu Asp Ser
47          25          30          35
49 aga tct gtt cag gga gaa ctt ggg tgg ata gca agc cct ctg gaa gga      198
50 Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro Leu Glu Gly
51          40          45          50
53 ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat aca cca atc cga      246
54 Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn Thr Pro Ile Arg
55          55          60          65
57 acc tac caa gtg tgc aat gtg atg gaa ccc agc cag aat aac tgg cta      294
58 Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln Asn Asn Trp Leu
59          70          75          80

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61	cga act gat tgg atc acc cga gaa ggg gct cag agg gtg tat att gag	342
62	Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg Val Tyr Ile Glu	
63	85 90 95 100	
65	att aaa ttc acc ttg agg gac tgc aat agt ctt ccg ggc gtc atg ggg	390
66	Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Val Met Gly	
67	105 110 115	
69	act tgc aag gag acg ttt aac ctg tac tac tat gaa tca gac aac gac	438
70	Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp	
71	120 125 130	
73	aaa gag cgt ttc atc aga gag aac cag ttt gtc aaa att gac acc att	486
74	Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys Ile Asp Thr Ile	
75	135 140 145	
77	gct gct gat gag agc ttc acc caa gtg gac att ggt gac aga atc atg	534
78	Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly Asp Arg Ile Met	
79	150 155 160	
81	aag ctg aac acc gag atc cgg gat gta ggg cca tta agc aaa aag ggg	582
82	Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu Ser Lys Lys Gly	
83	165 170 175 180	
85	ttt tgc ctg gct ttt cag gat gtg ggg gcc tgc atc gcc ctg gta tca	630
86	Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val Ser	
87	185 190 195	
89	gtc cgt gtg ttc tat aaa aag tgt cca ctc aca gtc cgc aat ctg gcc	678
90	Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val Arg Asn Leu Ala	
91	200 205 210	
93	cag ttt cct gac acc atc aca ggg gct gat acg tct tcc ctg gtg gaa	726
94	Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser Ser Leu Val Glu	
95	215 220 225	
97	gtt cga ggc tcc tgt gtc aac aac tca gaa gag aaa gat gtg cca aaa	774
98	Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys Asp Val Pro Lys	
99	230 235 240	
101	atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc att ggc aac tgc	822
102	Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro Ile Gly Asn Cys	
103	245 250 255 260	
105	cta tgc aac gct ggg cat gag gag cgg agc gga gaa tgc caa gct tgc	870
106	Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu Cys Gln Ala Cys	
107	265 270 275	
109	aaa att gga tat tac aag gct ctc tcc acg gat gcc acc tgt gcc aag	918
110	Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala Thr Cys Ala Lys	
111	280 285 290	
113	tgc cca ccc cac agc tac tct gtc tgg gaa gga gcc acc tgc tgc acc	966
114	Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala Thr Ser Cys Thr	
115	295 300 305	
117	tgt gac cga ggc ttt ttc aga gct gac aac gat gct gcc tct atg ccc	1014
118	Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala Ala Ser Met Pro	
119	310 315 320	
121	tgc acc cgt cca cca tct gct ccc ctg aac ttg att tca aat gtc aac	1062
122	Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile Ser Asn Val Asn	
123	325 330 335 340	
125	gag aca tct gtg aac ttg gaa tgg agt agc cct cag aat aca ggt ggc	1110

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126	Glu	Thr	Ser	Val	Asn	Leu	Glu	Trp	Ser	Ser	Pro	Gln	Asn	Thr	Gly	Gly	
127					345					350					355		
129	cgc	cag	gac	att	tcc	tat	aat	gtg	gta	tgc	aag	aaa	tgt	gga	gct	ggt	1158
130	Arg	Gln	Asp	Ile	Ser	Tyr	Asn	Val	Val	Cys	Lys	Lys	Cys	Gly	Ala	Gly	
131					360					365					370		
133	gac	ccc	agc	aag	tgc	cga	ccc	tgt	gga	agt	ggg	gtc	cac	tac	acc	cca	1206
134	Asp	Pro	Ser	Lys	Cys	Arg	Pro	Cys	Gly	Ser	Gly	Val	His	Tyr	Thr	Pro	
135					375					380					385		
137	cag	cag	aat	ggc	ttg	aag	acc	acc	aaa	gtc	tcc	atc	act	gac	ctc	cta	1254
138	Gln	Gln	Asn	Gly	Leu	Lys	Thr	Thr	Lys	Val	Ser	Ile	Thr	Asp	Leu	Leu	
139					390					395					400		
141	gct	cat	acc	aat	tac	acc	ttt	gaa	atc	tgg	gct	gtg	aat	gga	gtg	tcc	1302
142	Ala	His	Thr	Asn	Tyr	Thr	Phe	Glu	Ile	Trp	Ala	Val	Asn	Gly	Val	Ser	
143	405						410					415				420	
145	aaa	tat	aac	cct	aac	cca	gac	caa	tca	gtt	tct	gtc	act	gtg	acc	acc	1350
146	Lys	Tyr	Asn	Pro	Asn	Pro	Asp	Gln	Ser	Val	Ser	Val	Thr	Val	Thr	Thr	
147					425					430					435		
149	aac	caa	gca	gca	cca	tca	tcc	att	gct	ttg	gtc	cag	gct	aaa	gaa	gtc	1398
150	Asn	Gln	Ala	Ala	Pro	Ser	Ser	Ile	Ala	Leu	Val	Gln	Ala	Lys	Glu	Val	
151					440					445					450		
153	aca	aga	tac	agt	gtg	gca	ctg	gct	tgg	ctg	gaa	cca	gat	cgg	ccc	aat	1446
154	Thr	Arg	Tyr	Ser	Val	Ala	Leu	Ala	Trp	Leu	Glu	Pro	Asp	Arg	Pro	Asn	
155					455					460					465		
157	ggg	gta	atc	ctg	gaa	tat	gaa	gtc	aag	tat	tat	gag	aag	gat	cag	aat	1494
158	Gly	Val	Ile	Leu	Glu	Tyr	Glu	Val	Lys	Tyr	Tyr	Glu	Lys	Asp	Gln	Asn	
159					470					475					480		
161	gag	cga	agc	tat	cgt	ata	ggt	cgg	aca	gct	gcc	agg	aac	aca	gat	atc	1542
162	Glu	Arg	Ser	Tyr	Arg	Ile	Val	Arg	Thr	Ala	Ala	Arg	Asn	Thr	Asp	Ile	
163	485					490					495				500		
165	aaa	ggc	ctg	aac	cct	ctc	act	tcc	tat	gtt	ttc	cac	gtg	cga	gcc	agg	1590
166	Lys	Gly	Leu	Asn	Pro	Leu	Thr	Ser	Tyr	Val	Phe	His	Val	Arg	Ala	Arg	
167					505					510					515		
169	aca	gca	gct	ggc	tat	gga	gac	ttc	agt	gag	ccc	ttg	gag	gtt	aca	acc	1638
170	Thr	Ala	Ala	Gly	Tyr	Gly	Asp	Phe	Ser	Glu	Pro	Leu	Glu	Val	Thr	Thr	
171					520					525					530		
173	aac	aca	gtg	cct	tcc	cgg	atc	att	gga	gat	ggg	gct	aac	tcc	aca	gtc	1686
174	Asn	Thr	Val	Pro	Ser	Arg	Ile	Ile	Gly	Asp	Gly	Ala	Asn	Ser	Thr	Val	
175					535					540					545		
177	ctt	ctg	gtc	tct	gtc	tcg	ggc	agt	gtg	gtg	ctg	gtg	gta	att	ctc	att	1734
178	Leu	Leu	Val	Ser	Val	Ser	Gly	Ser	Val	Val	Leu	Val	Val	Ile	Leu	Ile	
179					550					555					560		
181	gca	gct	ttt	gtc	atc	agc	cgg	aga	cgg	agt	aaa	tac	agt	aaa	gcc	aaa	1782
182	Ala	Ala	Phe	Val	Ile	Ser	Arg	Arg	Arg	Ser	Lys	Tyr	Ser	Lys	Ala	Lys	
183	565					570				575					580		
185	caa	gaa	gcg	gat	gaa	gag	aaa	cat	ttg	aat	caa	ggg	gta	aga	aca	tat	1830
186	Gln	Glu	Ala	Asp	Glu	Glu	Lys	His	Leu	Asn	Gln	Gly	Val	Arg	Thr	Tyr	
187					585					590					595		
189	gtg	gac	ccc	ttt	acg	tac	gaa	gat	ccc	aac	caa	gca	gtg	cga	gag	ttt	1878
190	Val	Asp	Pro	Phe	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Arg	Glu	Phe	

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191	600	605	610	
193 gcc aaa gaa att gac gca tcc tgc att aag att gaa aaa gtt ata gga				1926
194 Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly				
195	615	620	625	
197 gtt ggt gaa ttt ggt gag gta tgc agt ggg cgt ctc aaa gtg cct ggc				1974
198 Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly				
199	630	635	640	
201 aag aga gag atc tgt gtg gct atc aag act ctg aaa gct ggt tat aca				2022
202 Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr				
203	645	650	655	660
205 gac aaa cag agg aga gac ttc ctg agt gag gcc agc atc atg gga cag				2070
206 Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln				
207	665	670	675	
209 ttt gac cat ccg aac atc att cac ttg gaa ggc gtg gtc act aaa tgt				2118
210 Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Cys				
211	680	685	690	
213 aaa cca gta atg atc ata aca gag tac atg gag aat ggc tcc ttg gat				2166
214 Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp				
215	695	700	705	
217 gca ttc ctc agg aaa aat gat ggc aga ttt aca gtc att cag ctg gtg				2214
218 Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu Val				
219	710	715	720	
221 ggc atg ctt cgt ggc att ggg tct ggg atg aag tat tta tct gat atg				2262
222 Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met				
223	725	730	735	740
225 agc tat gtg cat cgt gat ctg gcc gca cgg aac atc ctg gtg aac agc				2310
226 Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser				
227	745	750	755	
229 aac ttg gtc tgc aaa gtg tct gat ttt ggc atg tcc cga gtg ctt gag				2358
230 Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu				
231	760	765	770	
233 gat gat ccg gaa gca gct tac acc acc agg ggt ggc aag att cct atc				2406
234 Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile				
235	775	780	785	
237 cgg tgg act gcg cca gaa gca att gcc tat cgt aaa ttc aca tca gca				2454
238 Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala				
239	790	795	800	
241 agt gat gta tgg agc tat gga atc gtt atg tgg gaa gtg atg tcg tac				2502
242 Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr				
243	805	810	815	820
245 ggg gag agg ccc tat tgg gat atg tcc aat caa gat gtg att aaa gcc				2550
246 Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala				
247	825	830	835	
249 att gag gaa ggc tat ccg tta ccc cct cca atg gac tgc ccc att gcg				2598
250 Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala				
251	840	845	850	
253 ctc cac cag ctg atg cta gac tgc tgg cag aag gag agg agc gac agg				2646
254 Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg				
255	855	860	865	

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257 cct aaa ttt ggg cag att gtc aac atg ttg gac aaa ctc atc cgc aac      2694
258 Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn
259      870                      875                      880
261 ccc aac agc ttg aag agg aca ggg acg gag agc tcc aga cct aac act      2742
262 Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr
263 885                      890                      895                      900
265 gcc ttg ttg gat gca agc tcc cct gaa ttc tct gct gtg gta tca gtg      2790
266 Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val
267      905                      910                      915
269 ggc gat tgg ctc cag gcc att aaa atg gac cgg tat aag gat aac ttc      2838
270 Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe
271      920                      925                      930
273 aca gct gct ggt tat acc aca cta gag gct gtg gtg cac gtg aac cag      2886
274 Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln
275      935                      940                      945
277 gag gac ctg gca aga att ggt atc aca gcc atc acg cac cag aat aag      2934
278 Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys
279      950                      955                      960
281 att ttg agc agt gtc cag gca atg cga acc caa atg cag cag atg cac      2982
282 Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met His
283 965                      970                      975                      980
285 ggc aga atg gtt ccc gtc tga gccagtactg aataaactca aaactcttga      3033
286 Gly Arg Met Val Pro Val
287      985
289 aattagttta cctcatccat gcactttaat tgaagaactg cacttttttt acttcgtctt      3093
290 cgccctctga aattaaagaa atgaaaaaaa aaaacaatat ctgcagcggt gcttggtgca      3153
291 cagattgctg aaactgtggg gcttacagaa atgactgccg gtcatttgaa tgagacctgg      3213
292 aacaaatcgt ttctcagaag tacttttctg ttcatcacca gtctgtaaaa tacatgtacc      3273
293 tatagaaata gaacactgcc tctgagtttt gatgctgtat ttgctgccag acactgagct      3333
294 tctgagacat ccctgattct ctctccattt ggaattacaa ccattgtatt ttgtttgtgg      3393
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296 aggactcagc tgtggg      3468
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300 <211> LENGTH: 986
301 <212> TYPE: PRT
302 <213> ORGANISM: Homo sapiens
304 <400> SEQUENCE: 2
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308 Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
309      20      25      30
311 Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
312      35      40      45
315 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
316      50      55      60
318 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
319 65      70      75      80
321 Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
322      85      90      95

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : A:\082368-009500US.txt

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23

**VERIFICATION SUMMARY**

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Input Set : A:\082368-009500US.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:34